

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101781, 841A
Source: IFW/6
Date Processed by STIC: 6/13/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/13/2006

PATENT APPLICATION: US/10/781,841A

TIME: 09:51:34

Input Set : A:\Q76526 Seq List.txt

Output Set: N:\CRF4\06132006\J781841A.raw

3 <110> APPLICANT: FUJIWARA, TSUTOMU
 4 WATANABE, TAKESHI
 5 HORIE, MASATO
 7 <120> TITLE OF INVENTION: HUMAN SKELETAL MUSCLE-SPECIFIC
 8 UMBIQUITIN-CONJUGATING ENZYME
 10 <130> FILE REFERENCE: Q-76526
 12 <140> CURRENT APPLICATION NUMBER: 10/781,841A
 13 <141> CURRENT FILING DATE: 2004-02-20
 15 <150> PRIOR APPLICATION NUMBER: 10/342,276
 16 <151> PRIOR FILING DATE: 2003-01-15
 18 <150> PRIOR APPLICATION NUMBER: 09/273,565
 19 <151> PRIOR FILING DATE: 1999-03-22
 21 <150> PRIOR APPLICATION NUMBER: 09/055,699
 22 <151> PRIOR FILING DATE: 1998-04-07
 24 <150> PRIOR APPLICATION NUMBER: 08/820,170
 25 <151> PRIOR FILING DATE: 1997-03-19
 27 <150> PRIOR APPLICATION NUMBER: JP 63410/1996
 28 <151> PRIOR FILING DATE: 1996-03-19
 30 <150> PRIOR APPLICATION NUMBER: JP 69163/1997
 31 <151> PRIOR FILING DATE: 1997-03-05
 33 <160> NUMBER OF SEQ ID NOS: 96
 35 <170> SOFTWARE: PatentIn Ver. 2.1
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 122
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 1
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 44 1 5 10 15
 46 Ser Gln Asp Lys Ala Pro Ser Val Ile Ser Arg Val Leu Lys Lys Asn
 47 20 25 30
 49 Asn Arg Asp Ser Ala Val Ala Ser Glu Tyr Glu Leu Val Gln Leu Leu
 50 35 40 45
 53 Pro Gly Glu Arg Glu Leu Thr Ile Pro Ala Ser Ala Asn Val Phe Tyr
 54 50 55 60
 56 Pro Met Asp Gly Ala Ser His Asp Phe Leu Leu Arg Gln Arg Arg Arg
 57 65 70 75 80
 59 Ser Ser Thr Ala Thr Pro Gly Val Thr Ser Gly Pro Ser Ala Ser Gly
 60 85 90 95
 62 Thr Pro Pro Ser Glu Gly Gly Gly Gly Ser Phe Pro Arg Ile Lys Ala
 63 100 105 110
 65 Thr Gly Arg Lys Ile Ala Arg Ala Leu Phe
 66 115 120

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68 <210> SEQ ID NO: 2
69 <211> LENGTH: 366
70 <212> TYPE: DNA
71 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
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76 gctccaagtg tcatcagtcg tgccttaag aaaaacaatc gtgactctgc agtggcttca 120
78 gagtatgagc tggtagcgt gctaccaggg gagcgagagc tgactatccc agcctcggct 180
80 aatgtattct accccatgga tggagcttca cacgatttcc tcctgcggca gcggcgaagg 240
82 tcctctactg ctacacctgg cgtcaccagt ggcccgctcg cctcaggaac tcctccgagt 300
84 gaggaggagg ggggctcctt tcccaggatc aaggccacag ggaggaagat tgcacgggca 360
86 ctgttc
89 <210> SEQ ID NO: 3
90 <211> LENGTH: 842
91 <212> TYPE: DNA
92 <213> ORGANISM: Homo sapiens
94 <220> FEATURE:
95 <221> NAME/KEY: CDS
96 <222> LOCATION: (28)..(393)
98 <400> SEQUENCE: 3
99 cccacgagcc gtatcatccg agtccag atg gag ttg ggg gaa gat ggc agt gtc 54
100 Met Glu Leu Gly Glu Asp Gly Ser Val
101 1 5
103 tat aag agc att ttg gtg aca agc cag gac aag gct cca agt gtc atc 102
104 Tyr Lys Ser Ile Leu Val Thr Ser Gln Asp Lys Ala Pro Ser Val Ile
105 10 15 20 25
108 agt cgt gtc ctt aag aaa aac aat cgt gac tct gca gtg gct tca gag 150
109 Ser Arg Val Leu Lys Lys Asn Asn Arg Asp Ser Ala Val Ala Ser Glu
110 30 35 40
112 tat gag ctg gta cag ctg cta cca ggg gag cga gag ctg act atc cca 198
113 Tyr Glu Leu Val Gln Leu Leu Pro Gly Glu Arg Glu Leu Thr Ile Pro
114 45 50 55
116 gcc tcg gct aat gta ttc tac ccc atg gat gga gct tca cac gat ttc 246
117 Ala Ser Ala Asn Val Phe Tyr Pro Met Asp Gly Ala Ser His Asp Phe
118 60 65 70
120 ctc ctg cgg cag cgg cga agg tcc tct act gct aca cct ggc gtc acc 294
121 Leu Leu Arg Gln Arg Arg Arg Ser Ser Thr Ala Thr Pro Gly Val Thr
122 75 80 85
124 agt ggc ccg tct gcc tca gga act cct ccg agt gag gga gga ggg ggc 342
125 Ser Gly Pro Ser Ala Ser Gly Thr Pro Pro Ser Glu Gly Gly Gly Gly
126 90 95 100 105
128 tcc ttt ccc agg atc aag gcc aca ggg agg aag att gca cgg gca ctg 390
129 Ser Phe Pro Arg Ile Lys Ala Thr Gly Arg Lys Ile Ala Arg Ala Leu
130 110 115 120
132 ttc tgaggaggaa gccccttttt ttacagaagt catggtgttc ataccagatg 443
133 Phe
135 tgggtagcca tcctgaatgg tggcaattat atcacattga gacagaaatt cagaaagggg 503
137 gccagccacc ctggggcagt gaagtgccac tggtttaccg gacagctgag aaatccagcc 563
139 ctgtcgggaa tgggtgtctta taaccaagtt ggatacctgt gtatagcttg ccaccttcca 623

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141 tgagtgcagc acacaggtag tgctggaaaa acgcatcagt ttctgattct tggccatata 683
 143 ctaacatgca agggccaagc aaaggcttca aggctctgag ccccagggca gaggggaatg 743
 145 gcaaaatgta ggtcctggca ggagctcttc ttcccactct ggggggtttct atcactgtga 803
 147 caacactaag ataataaacc aaaacactac ctgaattct 842

150 <210> SEQ ID NO: 4

151 <211> LENGTH: 193

152 <212> TYPE: PRT

153 <213> ORGANISM: Homo sapiens

155 <400> SEQUENCE: 4

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159 Asp Gln Glu Asp Ala Leu Leu Gly Ser Tyr Pro Val Asp Asp Gly Cys

160 20 25 30

162 Arg Ile His Val Ile Asp His Ser Gly Ala Arg Leu Gly Glu Tyr Glu

163 35 40 45

165 Asp Val Ser Arg Val Glu Lys Tyr Thr Ile Ser Gln Glu Ala Tyr Asp

166 50 55 60

168 Gln Arg Gln Asp Thr Val Arg Ser Phe Leu Lys Arg Ser Lys Leu Gly

169 65 70 75 80

171 Arg Tyr Asn Glu Glu Glu Arg Ala Gln Gln Glu Ala Glu Ala Ala Gln

172 85 90 95

174 Arg Leu Ala Glu Glu Lys Ala Gln Ala Ser Ser Ile Pro Val Gly Ser

175 100 105 110

177 Arg Cys Glu Val Arg Ala Ala Gly Gln Ser Pro Arg Arg Gly Thr Val

178 115 120 125

180 Met Tyr Val Gly Leu Thr Asp Phe Lys Pro Gly Tyr Trp Ile Gly Val

181 130 135 140

183 Arg Tyr Asp Glu Pro Leu Gly Lys Asn Asp Gly Ser Val Asn Gly Lys

184 145 150 155 160

187 Arg Tyr Phe Glu Cys Gln Ala Lys Tyr Gly Ala Phe Val Lys Pro Ala

188 165 170 175

190 Val Val Thr Val Gly Asp Phe Pro Glu Glu Asp Tyr Gly Leu Asp Glu

191 180 185 190

193 Ile

196 <210> SEQ ID NO: 5

197 <211> LENGTH: 579

198 <212> TYPE: DNA

199 <213> ORGANISM: Homo sapiens

201 <400> SEQUENCE: 5

202 atggaactgg agctgtatgg agttgacgac aagttctaca gcaagctgga tcaagaggat 60

204 ggcgtcctgg gctcctaccc tgtagatgac ggctgccgca tccacgtcat tgaccacagt 120

206 ggcgcccgcg ttggtgagta tgaggacgtg tcccgggtgg agaagtacac gatctcacia 180

208 gaagcctacg accagaggca agacacggtc cgctctttcc tgaagcgagc caagctcggc 240

210 cggtacaacg aggaggagcg ggctcagcag gaggccgagg ccgcccagcg cctggccgag 300

212 gagaaggccc aggccagctc catccccgtg ggcagccgct gtgaggtgag ggcgggcgga 360

214 caatccccctc gccggggcac cgtcatgtat gtaggtctca cagatttcaa gcctggctac 420

216 tggattgggtg tccgctatga tgagccactg gggaaaaatg atggcagtgat gaatgggaaa 480

218 cgctacttcg aatgccaggc caagtatggc gcctttgtca agccagcagt cgtgacgggtg 540

220 ggggacttcc cggaggagga ctacgggttg gacgagata 579

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223 <210> SEQ ID NO: 6
224 <211> LENGTH: 1015
225 <212> TYPE: DNA
226 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (274)..(852)
232 <400> SEQUENCE: 6
233 tgattggtca ggcacggagc aggaggcgagg ctgatagccc agcagcagca gcggcgggcgg 60
235 cggctgcgga gcgggtgtga ggcggctgga ccgcgctgca ggcacccgcg ggcgcggcaa 120
237 gatggaggtg acgggggtgt cggcaccacg gtgaccgttt tcatcagcag ctccctcagc 180
239 accttccgct ccgagaagcg atacagccgc agcctcacca tcgctgagtt caagtgtaaa 240
241 ctggagttgc tgggtgggcag ccctgcttcc tgc atg gaa ctg gag ctg tat gga 294
242                                     Met Glu Leu Glu Leu Tyr Gly
243                                     1           5
245 gtt gac gac aag ttc tac agc aag ctg gat caa gag gat gcg ctc ctg 342
246 Val Asp Asp Lys Phe Tyr Ser Lys Leu Asp Gln Glu Asp Ala Leu Leu
247          10           15           20
249 ggc tcc tac cct gta gat gac ggc tgc cgc atc cac gtc att gac cac 390
250 Gly Ser Tyr Pro Val Asp Asp Gly Cys Arg Ile His Val Ile Asp His
251          25           30           35
253 agt ggc gcc cgc ctt ggt gag tat gag gac gtg tcc cgg gtg gag aag 438
254 Ser Gly Ala Arg Leu Gly Glu Tyr Glu Asp Val Ser Arg Val Glu Lys
255 40           45           50           55
257 tac acg atc tca caa gaa gcc tac gac cag agg caa gac acg gtc cgc 486
258 Tyr Thr Ile Ser Gln Glu Ala Tyr Asp Gln Arg Gln Asp Thr Val Arg
259          60           65           70
261 tct ttc ctg aag cgc agc aag ctc ggc cgg tac aac gag gag gag cgg 534
262 Ser Phe Leu Lys Arg Ser Lys Leu Gly Arg Tyr Asn Glu Glu Glu Arg
263          75           80           85
265 gct cag cag gag gcc gag gcc gcc cag cgc ctg gcc gag gag aag gcc 582
266 Ala Gln Gln Glu Ala Glu Ala Ala Gln Arg Leu Ala Glu Glu Lys Ala
267          90           95           100
269 cag gcc agc tcc atc ccc gtg ggc agc cgc tgt gag gtg cgg gcg gcg 630
270 Gln Ala Ser Ser Ile Pro Val Gly Ser Arg Cys Glu Val Arg Ala Ala
271          105           110           115
273 gga caa tcc cct cgc cgg ggc acc gtc atg tat gta ggt ctc aca gat 678
274 Gly Gln Ser Pro Arg Arg Gly Thr Val Met Tyr Val Gly Leu Thr Asp
275 120           125           130           135
277 ttc aag cct ggc tac tgg att ggt gtc cgc tat gat gag cca ctg ggg 726
278 Phe Lys Pro Gly Tyr Trp Ile Gly Val Arg Tyr Asp Glu Pro Leu Gly
279          140           145           150
281 aaa aat gat ggc agt gtg aat ggg aaa cgc tac ttc gaa tgc cag gcc 774
282 Lys Asn Asp Gly Ser Val Asn Gly Lys Arg Tyr Phe Glu Cys Gln Ala
283          155           160           165
285 aag tat ggc gcc ttt gtc aag cca gca gtc gtg acg gtg ggg gac ttc 822
286 Lys Tyr Gly Ala Phe Val Lys Pro Ala Val Val Thr Val Gly Asp Phe
287          170           175           180
289 ccg gag gag gac tac ggg ttg gac gag ata tgacacctaa ggaattcccc 872

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290 Pro Glu Glu Asp Tyr Gly Leu Asp Glu Ile
291      185                      190
293 tgcttcagct cctagctcag ccactgactg cccctcctgt gtgtgcccat ggcccttttc 932
295 tcctgacccc attttaattt tattcatttt ttcctttgcc attgattttt gagactcatg 992
297 cattaaattc actagaaacc cag                                     1015
300 <210> SEQ ID NO: 7
301 <211> LENGTH: 128
302 <212> TYPE: PRT
303 <213> ORGANISM: Homo sapiens
305 <400> SEQUENCE: 7
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307      1          5          10          15
309 His Leu Thr Lys Lys Leu Leu Asp Leu Val Gln Gln Ser Cys Asn Tyr
310          20          25          30
312 Lys Gln Leu Arg Lys Gly Ala Asn Glu Ala Thr Lys Thr Leu Asn Arg
313          35          40          45
315 Gly Ile Ser Glu Phe Ile Val Met Ala Ala Asp Ala Glu Pro Leu Glu
316          50          55          60
318 Ile Ile Leu His Leu Pro Leu Leu Cys Glu Asp Lys Asn Val Pro Tyr
319          65          70          75          80
321 Val Phe Val Arg Ser Lys Gln Ala Leu Gly Arg Ala Cys Gly Val Ser
322          85          90          95
324 Arg Pro Val Ile Ala Cys Ser Val Thr Ile Lys Glu Gly Ser Gln Leu
325          100         105         110
327 Lys Gln Gln Ile Gln Ser Ile Gln Ser Ile Glu Arg Leu Leu Val
328          115         120         125
331 <210> SEQ ID NO: 8
332 <211> LENGTH: 384
333 <212> TYPE: DNA
334 <213> ORGANISM: Homo sapiens
336 <400> SEQUENCE: 8
337 atgactgagg ctgatgtgaa tccaaaggcc tatccccttg ccgatgccca cctcaccaag 60
339 aagctactgg acctcggtca gcagtcattg aactataagc agcttcggaa aggagccaat 120
341 gaggccacca aaacctcaa caggggcatc tctgagttca tcgtgatggc tgcagacgcc 180
343 gagccactgg agatcattct gcacctgccg ctgctgtgtg aagacaagaa tgtgccctac 240
345 gtgtttgtgc gtcceaagca ggccctgggg agagcctgtg gggctctccag gcctgtcatc 300
347 gcctgttctg tcaccatcaa agaaggctcg cagctgaaac agcagatcca atccattcag 360
349 cagtccattg aaaggctctt agtc                                     384
352 <210> SEQ ID NO: 9
353 <211> LENGTH: 1493
354 <212> TYPE: DNA
355 <213> ORGANISM: Homo sapiens
357 <220> FEATURE:
358 <221> NAME/KEY: CDS
359 <222> LOCATION: (95)..(478)
361 <400> SEQUENCE: 9
362 atccgtgtcc ttgcggtgct gggcagcaga ccgtccaaac cgacacgcgt ggtatcctcg 60
364 cgggtgtccg caagagacta ccaagacaga cgct atg act gag gct gat gtg aat 115
365                               Met Thr Glu Ala Asp Val Asn

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; Xaa Pos. 2,9,13,15,16,20

Seq#:48; Xaa Pos. 11,13

Seq#:49; Xaa Pos. 9

Seq#:51; Xaa Pos. 3,14,23

Seq#:52; Xaa Pos. 20

Seq#:58; Xaa Pos. 1,2

Seq#:70; Xaa Pos. 5

Seq#:79; Xaa Pos. 2,3,6,11

VERIFICATION SUMMARY

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Input Set : A:\Q76526 Seq List.txt

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L:4385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
M:341 Repeated in SeqNo=45
L:4427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:4442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:4467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
M:341 Repeated in SeqNo=51
L:4488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:16
L:4553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:4681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:4785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0